SEQUENCE LISTING

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<110> Min, Wang
      Liu, Yingmei
<120> THIOREDOXIN MUTANTS AND USES THEREOF
<130> 21108.0021U2
<140> 10/523,343
<141>
<150> PCT/US03/22847
<151> 2002-07-02
<150> 60/401,073
<151> 2002-09-02
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Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp Cys
Gly Pro Cys Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu Lys
Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Cys Gln Asp
                        55
                                             60
Val Ala Ser Glu Cys Glu Val Lys Cys Met Pro Thr Phe Gln Phe Phe
                    70
Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys
                                    90
Leu Glu Ala Thr Ile Asn Glu Leu Val
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60

120

synthetic construct

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ttotttoatt coctototga aaagtattoo aacgtgatat toottgaagt agatgtggat
                                                                        180
gactgtcagg atgttgcttc agagtgtgaa gtcaaatgca tgccaacatt ccagtttttt
                                                                        240
aagaagggac aaaaggtggg tgaattttct ggagccaata aggaaaagct tgaagccacc
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attaatgaat tagtctaa
                                                                        318
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                                                                        120
ttctttcatt ccctctctga aaagtattcc aacgtgatat tccttgaagt agatgtggat
                                                                        180
gactgtcagg atgttgcttc agagtgtgaa gtcaaatgca tgccaacatt ccaqtttttt
                                                                        240
aagaagggac aaaaggtggg tgaattttct ggagccaata aggaaaaqct tqaaqccacc
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attaatgaat tagtctaa
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aaacttgtag tagttgactt ctcagccacg tggtgtgggc ctcgcaaaat gatcaagcct
                                                                        120
ttctttcatt ccctctctga aaagtattcc aacgtgatat tccttgaagt agatqtqqat
                                                                        180
gactgtcagg atgttgcttc agagtgtgaa gtcaaatgca tgccaacatt ccaqtttttt
                                                                        240
aagaagggac aaaaggtggg tgaattttct ggagccaata aggaaaagct tgaagccacc
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attaatgaat tagtctaa
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<210> 8
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Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu
            20
                                25
Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro
                            40
Ala Arg Thr Ile Tyr Thr Thr Arg Ile Ser Leu Thr Thr Phe Asn Ile
Gln Asp Gly Pro Asp Phe Gln Asp Arg Val Val Asn Ser Glu Thr Pro
                    70
                                        75
Val Val Asp Phe His Ala Gln Trp Cys Gly Pro Cys Lys Ile Leu
                                    90
Gly Pro Arg Leu Glu Met Val Ala Lys Gln His Gly Lys Val Val Met
                                105
Ala Lys Val Asp Ile Asp Asp His Thr Asp Leu Ala Ile Glu Tyr Glu
                            120
Val Ser Ala Val Pro Thr Val Leu Ala Met Lys Asn Gly Asp Val Val
                        135
Asp Lys Phe Val Gly Ile Lys Asp Glu Asp Gln Leu Glu Ala Phe Leu
                                                            160
                                        155
Lys Lys Leu Ile Gly
<210> 10
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Met Ala Gln Arg Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser
Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu
                                25
Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro
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40 Ala Arg Thr Ile Tyr Thr Thr Arg Ile Ser Leu Thr Thr Phe Asn Ile 55 60 Gln Asp Gly Pro Asp Phe Gln Asp Arg Val Val Asn Ser Glu Thr Pro Val Val Asp Phe His Ala Gln Trp Ser Gly Pro Cys Lys Ile Leu 90 Gly Pro Arg Leu Glu Met Val Ala Lys Gln His Gly Lys Val Val Met 105 Ala Lys Val Asp Ile Asp Asp His Thr Asp Leu Ala Ile Glu Tyr Glu 120 Val Ser Ala Val Pro Thr Val Leu Ala Met Lys Asn Gly Asp Val Val 135 Asp Lys Phe Val Gly Ile Lys Asp Glu Asp Gln Leu Glu Ala Phe Leu Lys Lys Leu Ile Gly 165 <210> 11 <211> 165 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence:/note = synthetic construct Met Ala Gln Arg Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser 10 Arg Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu 25 Gln Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro 40 Ala Arg Thr Ile Tyr Thr Thr Arg Ile Ser Leu Thr Thr Phe Asn Ile 55 Gln Asp Gly Pro Asp Phe Gln Asp Arg Val Val Asn Ser Glu Thr Pro Val Val Asp Phe His Ala Gln Trp Cys Gly Pro Ser Lys Ile Leu 90 Gly Pro Arg Leu Glu Met Val Ala Lys Gln His Gly Lys Val Val Met 105 Ala Lys Val Asp Ile Asp Asp His Thr Asp Leu Ala Ile Glu Tyr Glu 120 Val Ser Ala Val Pro Thr Val Leu Ala Met Lys Asn Gly Asp Val Val 135 Asp Lys Phe Val Gly Ile Lys Asp Glu Asp Gln Leu Glu Ala Phe Leu 150 155 Lys Lys Leu Ile Gly <210> 12 <211> 502 <212> DNA <213> Artificial Sequence

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cagggtcagt ggccacccct cacttccaga qccctgcaga ccccacaatg cagtcctggt
                                                                       120
ggcctgactg taacacccaa cccagcccgg acaatataca ccacgaggat ctccttgaca
                                                                       180
                                                                       240
acctttaata tccaggatgg acctgacttt caagaccgag tggtcaacag tgagacacca
                                                                       300
gtggttgtgg atttccacgc acagtggtgt ggaccctgca agatcctggg gccgaggtta
gagaagatgg tggccaagca gcacgggaag gtggtgatgg ccaaggtgga tattgatgac
                                                                       360
cacacagacc tegecattga gtatgaggtg teageggtge ceaetgtget ggecatgaag
                                                                       420
aatggggacg tggtggacaa gtttgtgggc atcaaggatg aggatcagtt ggaggccttc
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                                                                       502
ctgaagaagc tgattggctg ac
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cagggtcagt ggccacccct cacttccaga gccctgcaga ccccacaatg cagtcctggt
                                                                       120
ggcctgactg taacacccaa cccagcccgg acaatataca ccacgaggat ctccttgaca
                                                                       180
acctttaata tccaggatgg acctgacttt caagaccgag tggtcaacag tgagacacca
                                                                       240
gtqqttqtqq atttccacqc acaqtqqaqt qqaccctqca aqatcctqqq qccqaqqtta
                                                                       300
gagaagatgg tggccaagca gcacgggaag gtggtgatgg ccaaggtgga tattgatgac
                                                                       360
cacacagacc tegecattga gtatgaggtg teageggtge ceaetgtget ggecatgaag
                                                                       420
aatggggacg tggtggacaa gtttgtgggc atcaaggatg aggatcagtt ggaggccttc
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                                                                       502
ctgaagaagc tgattggctg ac
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cagggtcagt ggccacccct cacttccaga gccctgcaga ccccacaatg cagtcctggt
                                                                       120
ggcctgactg taacacccaa cccagcccgg acaatataca ccacgaggat ctccttgaca
                                                                       180
acctttaata tccaggatgg acctgacttt caagaccgag tggtcaacag tgagacacca
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gtggttgtgg atttccacgc acaqtgqtqt qqacccaqca aqatcctqqq qccqaqqtta
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gagaagatgg tggccaagca gcacgggaag gtggtgatgg ccaaggtgga tattgatgac
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cacacagacc tegecattga gtatgaggtg teageggtge ceaetgtget ggecatgaag
                                                                       420
aatggggacg tggtggacaa gtttgtgggc atcaaggatg aggatcagtt ggaggccttc
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Cys Gly Pro Cys
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Xaa Gly Pro Cys
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Cys Gly Pro Xaa
<210> 18
<211> 105
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Ala Ala Gly Asp Lys Leu Val Val Asp Phe Ser Ala Thr Trp Ser
                                25
Gly Pro Cys Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu Lys
                            40
Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Asp Cys Gln Asp
                        55
Val Ala Ser Glu Ser Glu Val Lys Cys Met Pro Thr Phe Gln Phe Phe
                    70
                                        75
Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys
                85
Leu Glu Ala Thr Ile Asn Glu Leu Val
            100
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Ala Ala Gly Asp Lys Leu Val Val Asp Phe Ser Ala Thr Trp Cys
Gly Pro Ser Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu Lys
                            40
Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Cys Gln Asp
                        55
Val Ala Ser Glu Ser Glu Val Lys Cys Met Pro Thr Phe Gln Phe Phe
Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys
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<212> PRT

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Thr Glu Arg Lys Ser
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<221> misc_RNA
<223> double stranded
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gccuuucuuu cauucccuc
                                                                          19
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<223> double stranded
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ugcaguccug guggccuga
                                                                          19
<210> 24
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<223> double stranded
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cgaagcgagc caagggcaa
                                                                         19
<210> 25
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<210><211><212><212><213>	79	
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	32 laaaa cagteetget eeegateege tteaceatee teaagettea agatggtgaa legag ageaagaeg	60 79
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<210><211><211><212><213>	79	
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